AMENDMENTS TO THE SPECIFICATION

Please amend the second complete paragraph on page 42 as follows:

Moreover, the nucleotide sequence determined from the cloning of the subject RAP-binding proteins from a human cell line will further allow for the generation of probes designed for use in identifying homologs in other human cell types, as well as RAP-BP homologs (e.g. orthologs) from other mammals. For example, by identifying highly conserved nucleotides sequence through comparison of the mammalian RAPT1 genes with the yeast TOR genes, it will be possible to design degenerate primers for isolating RAPT1 homologs from virtually any eukaryotic cell. For instance, alignment of the mouse RAPT1 gene sequence and the yeast DRR-1 and TOR2 sequences, we have determined that optimal primers for isolating RAPT1 homologs from other mammalian homologs, as well as from pathogenic fungi, include the primers GRGAYTTRAWBGABGCHYAMGAWTGG (SEQ ID NO: 31), CAAGCBTGGGAYMTYMTYTAYTATMAYGTBTTCAG (SEQ ID NO: 32), and GAYYBGARTTGGCTGTBCCHGG (SEQ ID NO: 33).

Please amend the first complete paragraph on page 67 as follows:

In order to clone homologs of the RAPT1 genes from human pathogen Candida, degenerate oligonucleotides based on the conserved regions of the RAPT1 and TOR proteins were designed and used to amplify C. albicans cDNA in .lambda.ZAP (strain 3153A). The amplification consisted of 30 cycles of 94 °C for 1 minute, 55 °C for 1 minute and 72 °C for 1 minute with the PCR amplimers

GGNAARGCNCAYCCNCARGC (SEQ ID NO: 29), and

ATNGCNGGRTAYTGYTGDATNTC (SEQ ID NO: 30). The PCR reactions were separated on a 2.5% low melting agarose gel, that identified a sizable fragment. The fragment was eluted and cloned into pCRII (TA cloning system, Invitrogen corporation).